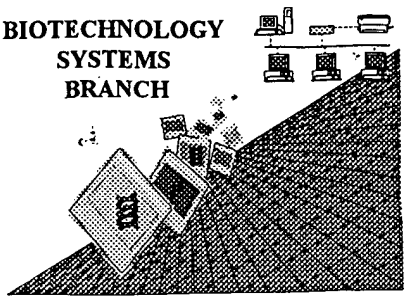
BIOTECHNOLOGY
SYSTEMS
BRANCH



NA

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/700,129

Source: PCT/09

Date Processed by STIC: 9/5/2001

BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/700,179

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/700,179

DATE: 09/05/2001
TIME: 13:29:02

Input Set : A:\ES.txt
Output Set: N:\CRF3\09052001\I700179.raw

Does Not Comply
Corrected Diskette Needed

```
     4 <110> APPLICANT: The University of Queensland
     5       National Institute of Biological Standards and Control
     7 <120> TITLE OF INVENTION: Novel anti-fibrinolytic agents
     9 <130> FILE REFERENCE: Textilinins
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/700,179
C--> 12 <141> CURRENT FILING DATE: 2001-07-27
    14 <150> PRIOR APPLICATION NUMBER: AU PP3450
    15 <151> PRIOR FILING DATE: 1999-05-11
    17 <160> NUMBER OF SEQ ID NOS: 44
    19 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

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  1010 <210> SEQ ID NO: 44
  1011 <211> LENGTH: 60
  1012 <212> TYPE: PRT
  1013 <213> ORGANISM: Pseudonaja textilis
  1015 <400> SEQUENCE: 44
  1016 Met Ser Ser Gly Gly Leu Leu Leu Leu Leu Gly Leu Leu Thr Leu Trp
  1017                -20                 -15                 -10
  1019 Glu Val Leu Thr Pro Val Ser Ser Lys Asp Arg Pro Glu Leu Cys Glu
  1020             -5                  -1   1                   5
  1022 Leu Pro Pro Asp Thr Gly Pro Cys Arg Val Arg Ser Pro Ser Phe Tyr
  1023      10                  15                  20
  1025 Tyr Asn Pro Asp Glu Gln Lys Cys Leu Glu Phe Ile
  1026  25                  30                  35
E--> 1035 (xv) delete
```

see p. 2

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate sense primer

<400> 27
atgaargaya grcchgaryt ngar 24

see item 9 on Eva Summary Sheet

VERIFICATION SUMMARY DATE: 09/05/2001
PATENT APPLICATION: **US/09/700,179** TIME: 13:29:03

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\09052001\I700179.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:531 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:598 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23
L:732 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:25
L:769 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:769 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1035 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1035 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1035 M:252 E: No. of Seq. differs, <211>LENGTH:Input:60 Found:61 SEQ:44